

M. Rao

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JUL 12 2000

TECH CENTER 1600/2900

1652

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7/13/00

#11

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/165,522

DATE: 06/26/2000
TIME: 12:25:14

Input Set : A:\Sequence
Output Set: N:\CRF3\06262000\I165522.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Davis, Roger J.
7 Flavell, Richard A.
8 Rakic, Pasko
9 Whitmarsh, Alan
10 Kuan, Chia-Yi
11 Yang, Di
13 (ii) TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
15 (iii) NUMBER OF SEQUENCES: 24
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Fish & Richardson P.C.
19 (B) STREET: 225 Franklin Street
20 (C) CITY: Boston
21 (D) STATE: MA
22 (E) COUNTRY: USA
23 (F) ZIP: 02110-2804
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Diskette
27 (B) COMPUTER: IBM Compatible
28 (C) OPERATING SYSTEM: Windows 95
29 (D) SOFTWARE: FastSEQ for Windows Version 2.0b
C--> 31 (vi) CURRENT APPLICATION DATA:
C--> 32 (A) APPLICATION NUMBER: US/09/165,522
C--> 33 (B) FILING DATE: 02-Oct-1998
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 60/060,995
37 (B) FILING DATE: 03-OCT-1997
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Fasse, J. Peter
41 (B) REGISTRATION NUMBER: 32,983
42 (C) REFERENCE/DOCKET NUMBER: 10363/005001
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 617/542-5070
46 (B) TELEFAX: 617/542-8906
47 (C) TELEX: 200154
49 (2) INFORMATION FOR SEQ ID NO: 1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 1505 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear
W--> 57 (ii) MOLECULE TYPE: DNA
59 (ix) FEATURE:
60 (A) NAME/KEY: Coding Sequence
61 (B) LOCATION: 68..1459
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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65	TTATGCAAGA AACTGTTGAA TTAGACCCGT TTCCTATAGA TGAGAAACCA TACAAGCTGT	60
66	GGTATTT ATG AGC CTC CAT TTC TTA TAC TAC TGC AGT GAA CCA ACA TTG	109
67	Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu	
68	1 5 10	
70	GAT GTG AAA ATT GCC TTT TGT CAG GGA TTC GAT AAA CAA GTG GAT GTG	157
71	Asp Val Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val	
72	15 20 25 30	
74	TCA TAT ATT GCC AAA CAT TAC AAC ATG AGC AAA AGC AAA GTT GAC AAC	205
75	Ser Tyr Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn	
76	35 40 45	
78	CAG TTC TAC AGT GTG GAA GTG GGA GAC TCA ACC TTC ACA GTT CTC AAG	253
79	Gln Phe Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys	
80	50 55 60	
82	CGC TAC CAG AAT CTA AAG CCT ATT GGC TCT GGG GCT CAG GGC ATA GTT	301
83	Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val	
84	65 70 75	
86	TGT GCC GCG TAT GAT GCT GTC CTT GAC AGA AAT GTG GCC ATT AAG AAG	349
87	Cys Ala Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys	
88	80 85 90	
90	CTC AGC AGA CCC TTT CAG AAC CAA ACA CAT GCC AAG AGA GCG TAC CGG	397
91	Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg	
92	95 100 105 110	
94	GAG CTG GTC CTC ATG AAG TGT GTG AAC CAT AAA AAC ATT ATT AGT TTA	445
95	Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu	
96	115 120 125	
98	TTA AAT GTC TTC ACA CCC CAG AAA ACG CTG GAG GAG TTC CAA GAT GTT	493
99	Leu Asn Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val	
100	130 135 140	
102	TAC TTA GTA ATG GAA CTG ATG GAT GCC AAC TTA TGT CAA GTG ATT CAG	541
103	Tyr Leu Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln	
104	145 150 155	
106	ATG GAA TTA GAC CAT GAG CGA ATG TCT TAC CTG CTG TAC CAA ATG TTG	589
107	Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu	
108	160 165 170	
110	TGT GGC ATT AAG CAC CTC CAT TCT GCT GGA ATT ATT CAC AGG GAT TTA	637
111	Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu	
112	175 180 185 190	
114	AAA CCA AGT AAC ATT GTA GTC AAG TCT GAT TGC ACA TTG AAA ATC CTG	685
115	Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu	
116	195 200 205	
118	GAC TTT GGA CTG GCC AGG ACA GCA GGC ACA AGC TTC ATG ATG ACT CCA	733
119	Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro	
120	210 215 220	
122	TAT GTG GTG ACA CGT TAT TAC AGA GCC CCT GAG GTC ATC CTG GGG ATG	781
123	Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met	
124	225 230 235	
126	GGC TAC AAG GAG AAC GTG GAT ATA TGG TCT GTG GGA TGC ATT ATG GGA	829
127	Gly Tyr Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly	
128	240 245 250	

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130 GAA ATG GTT CGC CAC AAA ATC CTC TTT CCA GGA AGG GAC TAT ATT GAC 877
 131 Glu Met Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp 270
 132 255 260 265 270
 134 CAG TGG AAT AAG GTA ATT GAA CAA CTA GGA ACA CCA TGT CCA GAA TTC 925
 135 Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe 285
 136 275 280 285
 138 ATG AAG AAA TTG CAA CCC ACA GTA AGA AAC TAT GTG GAG AAT CGG CCC 973
 139 Met Lys Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro 300
 140 290 295 300
 142 AAG TAT GCG GGA CTC ACC TTC CCC AAA CTC TTC CCA GAT TCC CTC TTC 1021
 143 Lys Tyr Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe 315
 144 305 310 315
 146 CCA GCG GAC TCC GAG CAC AAT AAA CTC AAA GCC AGC CAA GCC AGG GAC 1069
 147 Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp 330
 148 320 325 330
 150 TTG TTG TCA AAG ATG CTA GTG ATT GAC CCA GCA AAA AGA ATA TCA GTG 1117
 151 Leu Leu Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val 350
 152 335 340 345 350
 154 GAC GAC GCC TTA CAG CAT CCC TAC ATC AAC GTC TGG TAT GAC CCA GCC 1165
 155 Asp Asp Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala 365
 156 355 360 365
 158 GAA GTG GAG GCG CCT CCA CCT CAG ATA TAT GAC AAG CAG TTG GAT GAA 1213
 159 Glu Val Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu 380
 160 370 375 380
 162 AGA GAA CAC ACA ATT GAA GAA TGG AAA GAA CTT ATC TAC AAG GAA GTA 1261
 163 Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val 395
 164 385 390 395
 166 ATG AAT TCA GAA GAA AAG ACT AAA AAT GGT GTA GTA AAA GGA CAG CCT 1309
 167 Met Asn Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro 410
 168 400 405 410
 170 TCT CCT TCA GGT GCA GCA GTG AAC AGC AGT GAG AGT CTC CCT CCA TCC 1357
 171 Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser 425
 172 415 420 425 430
 174 TCG TCT GTC AAT GAC ATC TCC TCC ATG TCC ACC GAC CAG ACC CTG GCA 1405
 175 Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala 445
 176 435 440 445
 178 TCT GAC ACT GAC AGC AGC CTG GAA GCC TCG GCA GGA CCC CTG GGT TGT 1453
 179 Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys 460
 180 450 455 460
 182 TGC AGG TGACTAGCCG CCTGCCTGCG AAACCCAGCG TTCTTCAGGA GATGAT 1505
 183 Cys Arg
 186 (2) INFORMATION FOR SEQ ID NO: 2:
 188 (i) SEQUENCE CHARACTERISTICS:
 189 (A) LENGTH: 464 amino acids
 190 (B) TYPE: amino acid
 191 (D) TOPOLOGY: linear
 193 (ii) MOLECULE TYPE: protein
 195 (v) FRAGMENT TYPE: internal
 197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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 PATENT APPLICATION: US/09/165,522

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199 Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val
200 1 5 10 15
201 Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr
202 20 25 30
203 Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe
204 35 40 45
205 Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr
206 50 55 60
207 Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala
208 65 70 75 80
209 Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser
210 85 90 95
211 Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu
212 100 105 110
213 Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn
214 115 120 125
215 Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
216 130 135 140
217 Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu
218 145 150 155 160
219 Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly
220 165 170 175
221 Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro
222 180 185 190
223 Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe
224 195 200 205
225 Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val
226 210 215 220
227 Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr
228 225 230 235 240
229 Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met
230 245 250 255
231 Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp
232 260 265 270
233 Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys
234 275 280 285
235 Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr
236 290 295 300
237 Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala
238 305 310 315 320
239 Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu
240 325 330 335
241 Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp
242 340 345 350
243 Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val
244 355 360 365
245 Glu Ala Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu
246 370 375 380
247 His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn

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248 385          390          395          400
249 Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro
250          405          410          415
251 Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
252          420          425          430
253 Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
254          435          440          445
255 Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg
256          450          455          460

258 (2) INFORMATION FOR SEQ ID NO: 3:
260 (i) SEQUENCE CHARACTERISTICS:
261 (A) LENGTH: 2367 base pairs
262 (B) TYPE: nucleic acid
263 (C) STRANDEDNESS: double
264 (D) TOPOLOGY: linear
W--> 266 (ii) MOLECULE TYPE: DNA
268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
270 GAGAAATGGC GTGGCAGGGG ACCCAGCGAG CCCAGAGGGA TTTTGCCGCT GCTTCCTCTA 60
271 CCCCTGTATT TCACGCAGCT CTCTAAATTG ACTCAGCTCC AGGCTAGTGT GAGAAACACC 120
272 AACAGCAGGC CCATCTCAGA TCTTCACTAT GGCAACTTAT GCAAGAAACT GTTGAATTAG 180
273 ACCCGTTTCC TATAGATGAG AAACCATACA AGCTGTGGTA TTTATGAGCC TCCATTTCTT 240
274 ATACTACTGC AGTGAACCAA CATTTGGATGT GAAAATTGCC TTTTGTGTCAGG GATTTCGATAA 300
275 ACAAGTGGAT GTGTCAATATA TTGCCAAACA TTACAACATG AGCAAAAGCA AAGTTGACAA 360
276 CCAGTTCTAC AGTGTGGAAG TGGGAGACTC AACCTTCACA GTTCTCAAGC GCTACCAAGAA 420
277 TCTAAAGCCT ATTGGCTCTG GGGCTCAGGG CATAGTTTGT GCCGCGTATG ATGCTGTCTT 480
278 TGACAGAAAT GTGGCCATTA AGAAGCTCAG CAGACCCCTT CAGAACCAAA CACATGCCAA 540
279 GAGAGCGTAC CGGGAGCTGG TCCTCATGAA GTGTGTGAAC CATAAAAACA TTATTAGTTT 600
280 ATTAAATGTC TTACACACCC AGAAAACGCT GGAGGAGTTC CAAGATGTTT ACTTAGTAAT 660
281 GGAAGTATGAT GATGCCAACT TATGTCAAGT GATTTCAGATG GAATTAGACC ATGAGCGAAT 720
282 GTCTTACCTG CTGTACCAAA TGTGTGTGTT CATTAAGCAC CTCCATTCTG CTGGAATTAT 780
283 TCACAGGGAT TTAACACCAA GTAACATGTT AGTCAAGTCT GATTGCACAT TGAAAATCCT 840
284 GGACTTTGGA CTGGCCAGGA CAGCAGGCAC AAGCTTCATG ATGACTCCAT ATGTGGTGAC 900
285 ACCTTATTAC AGAGCCCTCT AGGTCACTCT GGGGATGGGC TACAAGGAGA ACGTGGATAT 960
286 ATGGTCTGTG GGATGCATTA TGGGAGAAAT GGTTCGCCAC AAAATCCTCT TTCCAGGAAG 1020
287 GGACTATATT GACCAGTGGA ATAAGGTAAT TGAACAACCTA GGAACACCAT GTCCAGAATT 1080
288 CATGAAGAAA TTGCAACCCA CAGTAAGAAA CTATGTGGAG AATCGGCCCA AGTATGCGGG 1140
289 ACTCACCTTC CCCAACTCT TCCAGATTC CCTCTTCCA GCGGACTCCG AGCACAATAA 1200
290 ACTCAAAGCC AGCCAAGCCA GGGACTTGTT GTCAAAGATG CTAGTGATTG ACCCAGCAAA 1260
291 AAGAAATATCA GTGGACGACG CCTTACAGCA TCCCTACATC AACGTCTGGT ATGACCCAGC 1320
292 CGAAGTGGAG GCGCTCCAC CTCAGATATA TGACAAGCAG TTGGATGAAA GAGAACACAC 1380
293 AATTGAAGAA TGGAAAGAAC TTATCTACAA GGAAGTAATG AATTGAGAAG AAAAGACTAA 1440
294 AAATGGTGTA GTAAAAGGAC AGCCTTCTCC TTCAGGTGCA GCAGTGAACA GCAGTGAGAG 1500
295 TCTCCCTCCA TCCTCGTCTG TCAATGACAT CTCCTCCATG TCCACCGACC AGACCTGGC 1560
296 ATCTGACACT GACAGCAGCC TGGAAAGCTC GGCAGGACCC CTGGGTTGTT GCAGGTGACT 1620
297 AGCCGCTGCG CTGCGAAACC CAGCGTCTCT CAGGAGATGA TGTGATGGAA CACACACACA 1680
298 CGCAGACACA CACACACACA CAAATGCAGA CACACAACAT CAAGAAAACA GCAAGGGAGA 1740
299 GAATCCAAGC CTAATAATTA ATAAATCTTT CAGCCTGCTT CTTCCTCAGG GTTCTGTATT 1800
300 GCAGCTAAGC TCAATGTAT ATTTAATTC TAGTTGCTCT TGCTTTGGTC TTCTTCCAAT 1860
301 GATGCTTACT ACAGAAAGCA AATCAGACAC AATTAGAGAA GCCTTTTCCA TAAAGTGTA 1920

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/165,522

DATE: 06/26/2000
TIME: 12:25:15

Input Set : A:\Sequence
Output Set: N:\CRF3\06262000\I165522.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:57 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[DNA]
L:266 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:319 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=[DNA]
L:520 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[DNA]
L:573 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:787 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9, Value=[DNA]
L:992 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11, Value=[DNA]
L:1206 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13, Value=[DNA]
L:1389 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15, Value=[DNA]
L:1529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17, Value=[DNA]
L:1543 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18, Value=[DNA]
L:1557 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19, Value=[DNA]
L:1571 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20, Value=[DNA]
L:1585 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21, Value=[DNA]
L:1599 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22, Value=[DNA]
L:1613 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=[DNA]
L:1627 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=[DNA]